CLAIMS

What is claimed is:

1. A method of analyzing genomic DNA in a sample, said method comprising:

providing first and second oligonucleotide primers, said first oligonucleotide primer being a 5′ variation generator, comprising a repeat sequence and at least one nucleotide inconsistent with the repeat pattern, said first oligonucleotide primer having at least one nucleotide positioned on the first oligonucleotide's 5′ end, and said second oligonucleotide primer being a 3′ fragment generator starting within such a genetic distance that amplification of the genomic DNA can be performed;

conducting a nucleic acid amplification on said genomic DNA in the sample using both the first and second oligonucleotide primers, thus producing DNA fragments based on repeat sequences on at least one end of the genomic DNA; and

analyzing an amplified product thus produced to determine its length.

2. The method according to claim 1 further comprising, conducting a second amplification on the products of the nucleic acid amplification, said second amplification being conducted using third and fourth oligonucleotide primers, said third and fourth oligonucleotide primers being elongated versions of said first and second oligonucleotide primers, respectively, enabling a selection of a sub-set of the DNA fragments amplified in the first amplification.

3. The method according to claim 1 or claim 2 further comprising digesting said amplified products with a restriction enzyme thus increasing the number of genetic polymorphisms detected in said genomic DNA and decreasing the sizes of the DNA fragments to be analysed for their length.

4. The method according to claim 1, 2, or 3 wherein the second oligonucleotide primer comprises an a-selective base such as inosine.

5. The method according to claim 2, 3 or 4 wherein the fourth oligonucleotide primer comprises an a-selective base such as inosine.

6. A method of determining the lineage of an individual by analyzing genomic DNA in a biological sample of the individual, said method comprising:

analyzing said genomic DNA in said biological sample to determine the presence of a repeat sequence;

determining the repeat sequence's length in number of nucleic acids; and

comparing the repeat sequence's length with a corresponding repeat sequence length of a putative ancestor of said individual.

7. The method according to claim 6 wherein the analysis of said genomic DNA in said sample comprises using a first oligonucleotide primer for performing a first amplification on said genomic DNA, said first oligonucleotide primer being a 5' variation generator and comprising a repeat sequence and at least one non-repeat nucleotide on the first oligonucleotide's 5' end.

8. A kit of parts for analyzing genomic DNA in a sample, said kit of parts comprising:

first and second oligonucleotide primers for performance of a first nucleic acid amplification on said genomic DNA, said first oligonucleotide primer being a 5' variation generator, and comprising a repeat sequence and at least one non-repeat nucleotide on the first oligonucleotide's 5' end, and said second oligonucleotide primer being a 3' fragment generator.

9. The kit of parts of claim 8 further comprising:

third and fourth oligonucleotide primers, said third oligonucleotide primer comprising the oligonucleotide sequence of said first oligonucleotide primer together with further nucleotides, and said fourth oligonucleotide primer comprising the oligonucleotide sequence of said second oligonucleotide primers together with further nucleotides.

10. The kit of parts of claim 7 further comprising at least one restriction enzyme.

11. The method according to claim 9 or claim 10 wherein at least one of the further nucleotides of the fourth oligonucleotide primer comprises an a-selective base such as inosine.

12. A method of analyzing genomic DNA in a sample, said method comprising:

providing first and second oligonucleotide primers for performance of a first polymerase chain reaction amplification on said genomic DNA, said first oligonucleotide primer being a 5' variation generator, and comprising a repeat sequence and at least one non-repeat nucleotide on the first oligonucleotide's 5' end, and said second oligonucleotide primer being a 3' fragment generator comprising at least one a-selective base such as inosine;

conducting said first amplification of said genomic DNA at a relatively low annealing temperature using both the first and second oligonucleotide primers, said first amplification being conducted under conditions such that neither the first nor the second oligonucleotide primer alone can amplify DNA, thus producing DNA fragments based on repeat sequences on one end of the genomic DNA, and other sequences based on the opposite end of the genomic DNA;

optionally diluting the reaction products of the first amplification;

conducting a second amplification on the reaction products of the first amplification, said second amplification being conducted using third and fourth oligonucleotide primers, said third and fourth oligonucleotide primers being elongated versions of said first and second oligonucleotide primers, respectively, enabling amplification at relatively higher annealing temperatures, and enabling a selection of a sub-set of the DNA fragments amplified in the first amplification; and

analyzing the sub-set of amplified products.

13. The method according to claim 12 further comprising digesting the amplified products of the first or second amplification with a restriction enzyme thus increasing the number of genetic polymorphisms detected in said genomic DNA and decreasing the sizes of the DNA fragments to be analyzed for their length.